GNE-0230R1C23

PATENT

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Applicant	:	Eaton, et al.
Appl. No.	:	10/063,534
Filed	:	May 2, 2002
For	:	ANTIBODIES TO A POLYPEPTIDE ENCODED BY A NUCLEIC ACID OVEREXPRESSED IN KIDNEY TUMOR AND UNDEREXPRESSED IN LUNG TUMOR (as amended)
Examiner	:	Seharaseyon, J.
Group Art Unit	:	1647

RESPONSE TO NOTICE TO COMPLY

Commissioner for Patents
P.O. Box 1450
Alexandria, VA 22313-1450

Dear Sir:

This Response to the Notice to Comply conforms the Sequence Listing to the rules of practice specified by the United States Patent and Trademark Office. Submitted herewith is a paper copy of the Sequence Listing and a copy of the Notice to Comply.

Please enter the attached sequence listing in the above-referenced application.

VERIFICATION UNDER 37 C.F.R. §1.821(f) & (g)

The sequences appearing in the attached Sequence Listing were included in the application as filed. Pursuant to 37 C.F.R. §1.821(g), no new matter is being added herewith. As required under 37 C.F.R. §1.821(f), I hereby verify that the data on the disk previously submitted and the paper copy of the Sequence Listing are identical.

Applicants believe this response to Notice to Comply brings the present application into compliance with the Sequence Listing requirements. A copy of the Notice to Comply is also submitted herewith.

Please charge any additional fees, including any fees for additional extension of time, or credit overpayment to Deposit Account No. 11-1410.
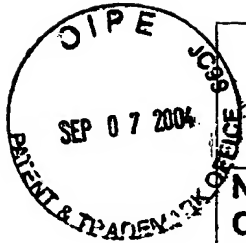
Respectfully submitted,

KNOBBE, MARTENS, OLSON & BEAR, LLP

Dated: _Sept. 2, 2004_

By: _AnneMarie Kaiser_

AnneMarie Kaiser
Registration No. 37,649
Attorney of Record
Customer No. 30,313
(619) 235-8550

S:\DOCS\BSG\BSG-1357.DOC
081304

Notice to Comply	Application No.	Applicant(s)
	10/063 534	EATON ET AL
	Examiner	Art Unit
	J. Seharaseyn	1647

NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES

Applicant must file the items indicated below within the time period set the Office action to which the Notice is attached to avoid abandonment under 35 U.S.C. § 133 (extensions of time may be obtained under the provisions of 37 CFR 1.136(a)).

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 C.F.R. 1.821 - 1.825 for the following reason(s):

☐ 1. This application clearly fails to comply with the requirements of 37 C.F.R. 1.821-1.825. Applicant's attention is directed to the final rulemaking notice published at 55 FR 18230 (May 1, 1990), and 1114 OG 29 (May 15, 1990). If the effective filing date is on or after July 1, 1998, see the final rulemaking notice published at 63 FR 29620 (June 1, 1998) and 1211 OG 82 (June 23, 1998).

☒ 2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 C.F.R. 1.821(c).

☐ 3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 C.F.R. 1.821(e).

☐ 4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 C.F.R. 1.822 and/or 1.823, as indicated on the attached copy of the marked -up "Raw Sequence Listing."

☐ 5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A Substitute computer readable form must be submitted as required by 37 C.F.R. 1.825(d).

☐ 6. The paper copy of the "Sequence Listing" is not the same as the computer readable from of the "Sequence Listing" as required by 37 C.F.R. 1.821(e).

☐ 7. Other:

Applicant Must Provide:
☐ An initial or substitute computer readable form (CRF) copy of the "Sequence Listing".

☒ An initial or substitute paper copy of the "Sequence Listing", as well as an amendment directing its entry into the specification.

☒ A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 C.F.R. 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d).

For questions regarding compliance to these requirements, please contact:

For Rules Interpretation, call (703) 308-4216 or (703) 308-2923
For CRF Submission Help, call (703) 308-4212 or 308-2923
PatentIn Software Program Support
  Technical Assistance..703-287-0200
  To Purchase PatentIn Software........................703-306-2600

PLEASE RETURN A COPY OF THIS NOTICE WITH YOUR REPLY

GenBank (Release 142, jun 2004)

494 100   0.0
P_AAF92072   Human PRO831 cDNA. 494 bp, cDNA, PAT 15-MAY-2001
ACCESSION   P_AAF92072
KEYWORDS   GENESEQ; Human; PRO protein; mapping; patent; patentdb (v200414,
             01-JUL-2004).
SOURCE   Homo sapiens.
  ORGANISM   Homo sapiens.
REFERENCE   1 (bases 1 to 494)
  AUTHORS   Eaton,D.L., Filvaroff,E., Gerritsen,M.E., Goddard,A.,
             Godowski,P.J. Grimaldi,C.J., Gurney,A.L., Watanabe,C.K.,
             Wood,W.I.
  TITLE   Eighty four nucleic acids encoding PRO polypeptides, useful in
             molecular biology, including use as hybridization probes, and in
             chromosome and gene mapping.
  JOURNAL   Patent: WO200116318-A2; Filing Date: 24-AUG-2000; 2000WO-US023328;
             Publication Date: 08-MAR-2001; Priority: 01-SEP-1999;
             99WO-US020111. 15-SEP-1999;   99WO-US021090. 07-DEC-1999;
             99US-0169495P. 09-DEC-1999;   99US-0170262P. 11-JAN-2000;
             2000US-0175481P. 18-FEB-2000; 2000WO-US004341. 18-FEB-2000;
             2000WO-US004342. 22-FEB-2000; 2000WO-US004414. 01-MAR-2000;
             2000WO-US005601. 03-MAR-2000; 2000US-0187202P. 21-MAR-2000;
             2000US-0191007P. 30-MAR-2000; 2000WO-US008439. 25-APR-2000;
             2000US-0199397P. 22-MAY-2000; 2000WO-US014042. 05-JUN-2000;
             2000US-0209832P; Assignee: (GETH) GENENTECH INC; Cross Reference:
             WPI; 2001-183260/18. P-PSDB; AAB87540; Patent Format: Claim 2; Fig
             29; 278pp; English.
COMMENT   The present sequence is the coding sequence for a human PRO
             polypeptide (secreted and transmembrane). The PRO protein, and PRO
             agonists, PRO antagonists or anti-PRO antibodies are useful for
             preparation of a medicament useful in the treatment of a condition
             which is responsive to the PRO protein, agonists, antagonists or
             anti-PRO antibodies. The PRO protein may also be employed as
             molecular weight markers for protein electrophoresis. The PRO
             coding sequence has applications in molecular biology, including
             use as hybridisation probes, and in chromosome and gene mapping
FEATURES   Location/Qualifiers
BASE COUNT   128 a   111 c   120 g   135 t
ORIGIN

494 100   0.0
AX092298   Sequence 29 from Patent WO0116318. 494 bp,
             DNA, linear, PAT 21-MAR-2001
ACCESSION   AX092298
VERSION   AX092298.1 GI:13444463
KEYWORDS   .
SOURCE   Homo sapiens (human)
  ORGANISM   Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Eaton,D.L., Filvaroff,E., Gerritsen,M.E., Goddard,A.,
             Godowski,P.J., Grimaldi,C.J., Gurney,A.L., Watanabe,C.K. and
             Wood,W.I.
  TITLE   Secreted and transmembrane polypeptides and nucleic acids encoding
             the same

FEATURES   Location/Qualifiers
    source   1..494
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
BASE COUNT
ORIGIN

493 100   0.0
P_AAA37028   Human PRO831 (UNQ471) cDNA sequence SEQ ID NO:21. 493 bp,
            cDNA, PAT 08-AUG-2000
ACCESSION   P_AAA37028
KEYWORDS   GENESEQ; Human; PRO polypeptide; membrane bound protein; receptor;
            diagnosis; transmembrane; secretion; immunoadhesion; pharmaceutical;
            screening; patent; patentdb (v200414, 01-JUL-2004).
SOURCE   Homo sapiens.
  ORGANISM Homo sapiens.
REFERENCE   1 (bases 1 to 493)
  AUTHORS   Baker,K., Goddard,A., Gurney,A.L., Smith,V., Watanabe,C.K.,
            Wood,W.I.
  TITLE   New mammalian DNA sequences encoding transmembrane, receptor or
            secreted PRO polypeptides, useful for screening of potential
            peptide or small molecule inhibitors of the relevant
            receptor/ligand interactions.
  JOURNAL   Patent: WO200012708-A2; Filing Date: 01-SEP-1999;   99WO-US020111;
            Publication Date: 09-MAR-2000; Priority: 01-SEP-1998;
            98US-0098716P. 01-SEP-1998;   98US-0098749P. 01-SEP-1998;
            98US-0098750P. 02-SEP-1998;   98US-0098803P. 02-SEP-1998;
            98US-0098821P. 02-SEP-1998;   98US-0098843P. 09-SEP-1998;
            98US-0099536P. 09-SEP-1998;   98US-0099596P. 09-SEP-1998;
            98US-0099598P. 09-SEP-1998;   98US-0099602P. 09-SEP-1998;
            98US-0099642P. 10-SEP-1998;   98US-0099741P. 10-SEP-1998;
            98US-0099754P. 10-SEP-1998;   98US-0099763P. 10-SEP-1998;
            98US-0099792P. 10-SEP-1998;   98US-0099808P. 10-SEP-1998;
            98US-0099812P. 10-SEP-1998;   98US-0099815P. 10-SEP-1998;
            98US-0099816P. 15-SEP-1998;   98US-0100385P. 15-SEP-1998;
            98US-0100388P. 15-SEP-1998;   98US-0100390P. 16-SEP-1998;
            98US-0100584P. 16-SEP-1998;   98US-0100627P. 16-SEP-1998;
            98US-0100661P. 16-SEP-1998;   98US-0100662P. 16-SEP-1998;
            98US-0100664P. 17-SEP-1998;   98US-0100683P. 17-SEP-1998;
            98US-0100684P. 17-SEP-1998;   98US-0100710P. 17-SEP-1998;
            98US-0100711P. 17-SEP-1998;   98US-0100919P. 17-SEP-1998;
            98US-0100930P. 18-SEP-1998;   98US-0100848P. 18-SEP-1998;
            98US-0100849P. 18-SEP-1998;   98US-0101014P. 18-SEP-1998;
            98US-0101068P. 18-SEP-1998;   98US-0101071P. 22-SEP-1998;
            98US-0101279P. 23-SEP-1998;   98US-0101471P. 23-SEP-1998;
            98US-0101472P. 23-SEP-1998;   98US-0101474P. 23-SEP-1998;
            98US-0101475P. 23-SEP-1998;   98US-0101476P. 23-SEP-1998;
            98US-0101477P. 23-SEP-1998;   98US-0101479P. 24-SEP-1998;
            98US-0101738P. 24-SEP-1998;   98US-0101741P. 24-SEP-1998;
            98US-0101743P. 24-SEP-1998;   98US-0101915P. 24-SEP-1998;
            98US-0101916P. 29-SEP-1998;   98US-0102207P. 29-SEP-1998;
            98US-0102240P. 29-SEP-1998;   98US-0102307P. 29-SEP-1998;
            98US-0102330P. 29-SEP-1998;   98US-0102331P. 30-SEP-1998;
            98US-0102484P. 30-SEP-1998;   98US-0102487P. 30-SEP-1998;

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          98US-0102570P.  30-SEP-1998;    98US-0102571P.  01-OCT-1998;
          98US-0102684P.  01-OCT-1998;    98US-0102687P.  02-OCT-1998;
          98US-0102965P.  06-OCT-1998;    98US-0103258P.  06-OCT-1998;
          98US-0103449P.  07-OCT-1998;    98US-0103314P.  07-OCT-1998;
          98US-0103315P.  07-OCT-1998;    98US-0103328P.  07-OCT-1998;
          98US-0103395P.  07-OCT-1998;    98US-0103396P.  07-OCT-1998;
          98US-0103401P.  08-OCT-1998;    98US-0103633P.  08-OCT-1998;
          98US-0103678P.  08-OCT-1998;    98US-0103679P.  08-OCT-1998;
          98US-0103711P.  14-OCT-1998;    98US-0104257P.  20-OCT-1998;
          98US-0104987P.  20-OCT-1998;    98US-0105000P.  20-OCT-1998;
          98US-0105002P.  21-OCT-1998;    98US-0105104P.  22-OCT-1998;
          98US-0105169P.  22-OCT-1998;    98US-0105266P.  26-OCT-1998;
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          98US-0105807P.  27-OCT-1998;    98US-0105881P.  27-OCT-1998;
          98US-0105882P.  27-OCT-1998;    98US-0106062P.  28-OCT-1998;
          98US-0106023P.  28-OCT-1998;    98US-0106029P.  28-OCT-1998;
          98US-0106030P.  28-OCT-1998;    98US-0106032P.  28-OCT-1998;
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          98US-0106248P.  29-OCT-1998;    98US-0106384P.  29-OCT-1998;
          98US-0108500P.  30-OCT-1998;    98US-0106464P.  03-NOV-1998;
          98US-0106856P.  03-NOV-1998;    98US-0106902P.  03-NOV-1998;
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          98US-0106932P.  03-NOV-1998;    98US-0106934P.  10-NOV-1998;
          98US-0107783P.  17-NOV-1998;    98US-0108775P.  17-NOV-1998;
          98US-0108779P.  17-NOV-1998;    98US-0108787P.  17-NOV-1998;
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          98US-0108802P.  17-NOV-1998;    98US-0108806P.  17-NOV-1998;
          98US-0108807P.  17-NOV-1998;    98US-0108867P.  17-NOV-1998;
          98US-0108925P.  18-NOV-1998;    98US-0108848P.  18-NOV-1998;
          98US-0108849P.  18-NOV-1998;    98US-0108850P.  18-NOV-1998;
          98US-0108851P.  18-NOV-1998;    98US-0108852P.  18-NOV-1998;
          98US-0108858P.  18-NOV-1998;    98US-0108904P; Assignee: (GETH )
          GENENTECH INC; Cross Reference: WPI; 2000-237871/20. P-PSDB;
          AAY99346; Patent Format: Claim 2; Fig 13; 773pp; English.
COMMENT    AAA37022 to AAA37144 encode the new isolated human transmembrane,
          receptor or secreted PRO polypeptides given in AAY99340 to AAY99462.
          The  transmembrane and receptor PRO proteins can be used for
          screening of  potential peptide or small molecule inhibitors of the
          relevant  receptor/ligand interactions. The polypeptides and
          nucleotide sequences  encoding then have various industrial
          applications, including uses as  pharmaceutical and diagnostic
          agents. AAA37145 to AAA37330 represent PCR  primers and
          hybridisation probes used in the isolation of the PRO  polypeptides
          from the present invention
FEATURES              Location/Qualifiers
BASE COUNT      127 a     111 c     120 g      135 t
ORIGIN

486 100    0.0
BC021104     Homo sapiens apelin, AGTRL1 ligand, mRNA (cDNA clone MGC:31846
             IMAGE:4586949), complete cds. 2673 bp,
             mRNA, linear, PRI 30-JUN-2004
ACCESSION    BC021104
VERSION      BC021104.1  GI:18088893
KEYWORDS     MGC.
SOURCE       Homo sapiens (human)
  ORGANISM   Homo sapiens
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          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 2673)
  AUTHORS   Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
          Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
          Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
          Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
          Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
          Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
          Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
          Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
          Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
          McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
          Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
          Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
          Fahey,J., Helton,E., Ketteman,M., Madan,A., Rodrigues,S.,
          Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
          Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
          Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
          Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E.,
          Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
    TITLE   Generation and initial analysis of more than 15,000 full-length
          human and mouse cDNA sequences
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
REFERENCE   2  (bases 1 to 2673)
  AUTHORS   Strausberg,R.
    TITLE   Direct Submission
  JOURNAL   Submitted (03-JAN-2002) National Institutes of Health, Mammalian
          Gene Collection (MGC), Cancer Genomics Office, National Cancer
          Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
          USA
   REMARK   NIH-MGC Project URL: http://mgc.nci.nih.gov
  COMMENT   Contact: MGC help desk
          Email: cgapbs-r@mail.nih.gov
          Tissue Procurement: DCTD/DTP
          cDNA Library Preparation: Rubin Laboratory
          cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
          DNA Sequencing by: Genome Sequence Centre,
          BC Cancer Agency, Vancouver, BC, Canada
          info@bcgsc.bc.ca
          Steve Jones, Sarah Barber, Mabel Brown-John, Yaron Butterfield,
          Andy Chan, Steve S. Chand, William Chow, Alison Cloutier, Ruth
          Featherstone, Malachi Griffith, Obi Griffith, Ran Guin, Nancy Liao,
          Kim MacDonald, Amara Masson, Mike R. Mayo, Josh Moran, Ryan Morin,
          Teika Olson, Diana Palmquist, Anca Petrescu, Anna Liisa Prahbu,
          Parvaneh Saeedi, JR Santos, Angelique Schnerch, Ursula Skalska,
          Duane Smailus, Jeff Stott, Miranda Tsai, George Yang, Jacquie
          Schein, Asim Siddiqui, Rob Holt, Marco Marra.

          Clone distribution: MGC clone distribution information can be found
          through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
          Series: IRAL Plate: 40 Row: f Column: 18
          This clone was selected for full length sequencing because it
          passed the following selection criteria: matched mRNA gi: 21314667.
FEATURES             Location/Qualifiers
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BASE COUNT
ORIGIN


468 100   0.0
P_AAX235184Human kidney aminopeptidase P genomic DNA fragment 2. 998 bp,
          DNA, PAT 23-JUN-1999
ACCESSION   P_AAX23518
KEYWORDS    GENESEQ; Aminopeptidase; human; AmP; gene therapy; treatment;
          AmP-deficiency; prenatal diagnosis; angioedema; antihypertensive
          agent; atherosclerosis; arterial stenosis; industrial protein feed;
          malabsorption syndrome; proteinaceous waste degradation; additive;
          immunohistochemistry;  patent; patentdb (v200414, 01-JUL-2004).
SOURCE      Homo sapiens.
  ORGANISM  Homo sapiens.
REFERENCE   1  (bases 1 to 49998)
  AUTHORS   Ryan,J.W.,  Sprinkle,T.J.C.,  Venema,R.C.
  TITLE     Nucleic acid encoding human aminopeptidase P.
  JOURNAL   Patent: WO9911799-A2; Filing Date: 02-SEP-1998;   98WO-US018426;
          Publication Date: 11-MAR-1999; Priority: 02-SEP-1997;
          97US-0057854P; Assignee: (MEDI-) MEDICAL COLLEGE GEORGIA RES INST;
          Cross Reference: WPI; 1999-205193/17; Patent Format: Claim 13; Page
          109-139; 201pp; English.
COMMENT     This invention describes the isolation of a novel human
          aminopeptidase P  (AmP). This protein is used to produce recombinant
          AmP and can be used  for gene therapy for treating AmP-deficiency
          conditions. Its fragments  are used as primers and probes to
          identify patients with homozygous and  heterozygous AmP deficiency,
          including prenatal diagnosis (patients  defective in AmP are at risk
          of developing angioedema if treated with  angiotensin-converting
          enzyme inhibitors), also as antisense inhibitors  in cases of
          excessive AmP expression. The product of the invention is  also used
          to identify AmP-expressing sequences in other animals and to
          generate transgenic animals, and comparisons of genomic sequences
          are  used to detect mutations. AmP inhibitors are potentially useful
          as  antihypertensive agents and to prevent or treat arterial
          (re)stenosis or  atherosclerosis. The structure of AmP is used to
          design synthetic  substrates, e.g. for use in AmP assays. AmP, which
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hydrolyzes N-terminal imido bonds, can be used to degrade
industrial protein feeds to free amino acids, to degrade
proteinaceous wastes, as additives in enzyme formulations used to
treat malabsorption syndrome and for studying its biological role.
Antibodies against AmP are used in immunohistochemical methods to
study AmP distribution

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FEATURES             Location/Qualifiers
BASE COUNT    12605 a  11725 c  11351 g  14317 t
ORIGIN
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468 100   0.0
HS454M7   Human DNA sequence from clone RP3-454M7 on chromosome Xq25-26.3,
            complete sequence. 151152 bp, DNA, linear, PRI 05-JUN-2003

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ACCESSION    AL022162
VERSION      AL022162.1  GI:3171881
KEYWORDS     HTG.
SOURCE       Homo sapiens (human)
  ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1  (bases 1 to 151152)
  AUTHORS    Pavitt,R.
  TITLE      Direct Submission
  JOURNAL    Submitted (05-JUN-2003) Wellcome Trust Sanger Institute, Hinxton,
            Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
            humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
COMMENT      On Jun 2, 1998 this sequence version replaced gi:2969945.
            --------------- Genome Center
            Center: Wellcome Trust Sanger Institute
            Center code: SC
            Web site: http://www.sanger.ac.uk
            Contact: humquery@sanger.ac.uk
            ---------------
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During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality }=
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by at least
one plasmid subclone or more than one M13 subclone; and the
assembly was confirmed by restriction digest, except on the rare
occasion of the clone being a YAC.
The following abbreviations are used to associate primary accession
numbers given in the feature table with their source databases:
Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information
on the WORMPEP database can be found at
http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence
was generated from part of bacterial clone contigs of human
chromosome X, constructed by the Sanger Centre Chromosome X Mapping
Group. Further information can be found at
http://www.sanger.ac.uk/HGP/ChrX
RP3-454M7 is from the library RPCI-3 constructed by the group of

```
                    Pieter de Jong. For further details see
                    http://www.chori.org/bacpac/home.htm
                    VECTOR: pCYPAC2
                    This sequence is the entire insert of clone RP3-454M7.
FEATURES                      Location/Qualifiers
     source               1..151152
                          /organism="Homo sapiens"
                          /mol_type="genomic DNA"
                          /db_xref="RZPD:RPCIP704M07454"
                          /db_xref="taxon:9606"
                          /chromosome="X"
                          /map="q25-26.3"
                          /clone="RP3-454M7"
                          /clone_lib="RPCI-3"
     gene                 767..35998
                          /gene="OCRL1"
     mRNA                 join(<767..877,1303..1392,2075..2195,2282..2443,
                          3992..4093,4621..4735,5826..5942,6041..6228,9214..9325,
                          10696..10805,12706..12841,18582..18692,19339..19504,
                          19759..19994,30444..30560,31621..31705,32328..32455,
                          33287..33398,33588..35998)
                          /gene="OCRL1"
                          /product="dJ454M7.1.1 (Lowe Oculocerebrorenal Syndrome)"
                          /note="variant 1
                          match: cDNAs: Em:M88162 Em:U57627 Em:M74161 Em:AF040094
                          match: ESTs: Em:AA368192 Em:AA704671 Em:AA515789
                          Em:AA102623 Em:AA126320 Em:T63686 Em:AA884344 Em:N92504
                          Em:AA044611 Em:AA188493 Em:AA743649 Em:AA836673 Em:R67320
                          Em:AA100629 Em:AA085500 Em:R94403 Em:AA056506 Em:AA034375
                          Em:AA142870 Em:AA150871 Em:T84251 Em:AA122020 Em:AA906612
                          Em:F07337 Em:AA628152 Em:AA878369 Em:AA640853 Em:AA189134
                          Em:AA044666 Em:AA740555 Em:R18793 Em:AA844284 Em:AA904845
                          Em:AA042798 Em:AA122019 Em:H53971 Em:W38961 Em:AA805220
                          Em:AA868822 Em:AA032176 Em:AA034374 Em:T84250 Em:N56932
                          Em:AA169401 Em:AA188849 Em:N46002 Em:AA056392 Em:H87857
                          Em:W52373 Em:AA587050 Em:AA100630 Em:T88888 Em:H27722
                          Em:AA186750 Em:R66483 Em:T28294"
                          /evidence=not_experimental
     CDS                  join(<769..877,1303..1392,2075..2195,2282..2443,
                          3992..4093,4621..4735,5826..5942,6041..6228,9214..9325,
                          10696..10805,12706..12841,18582..18692,19339..19504,
                          19759..19994,27786..27809,30444..30560,31621..31705,
                          32328..32455,33287..33398,33588..33712)
                          /gene="OCRL1"
                          /codon_start=1
                          /evidence=not_experimental
                          /product="dJ454M7.1.2 (variant 2)"
                          /protein_id="CAA18150.1"
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     CDS                  join(<769..877,1303..1392,2075..2195,2282..2443,
                          3992..4093,4621..4735,5826..5942,6041..6228,9214..9325,
                          10696..10805,12706..12841,18582..18692,19339..19504,
                          19759..19994,30444..30560,31621..31705,32328..32455,
                          33287..33398,33588..33712)
                          /gene="OCRL1"
                          /note="variant 1"
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                        /protein_id="CAA18151.1"
                        /db_xref="GI:4160528"
repeat_region      1586..1847
                        /note="MIR repeat: matches 2..262 of consensus"
repeat_region      2642..2940
                        /note="AluJb repeat: matches 1..302 of consensus"
repeat_region      6639..6933
                        /note="MER33 repeat: matches 1..323 of consensus"
repeat_region      7178..8315
                        /note="L1PA2 repeat: matches 5000..6146 of consensus"
repeat_region      11225..11294
                        /note="MER5B repeat: matches 109..178 of consensus"
repeat_region      11345..11657
                        /note="AluYb8 repeat: matches 1..310 of consensus"
repeat_region      11736..11797
                        /note="31 copies 2 mer tt 72% conserved"
repeat_region      12436..12562
                        /note="L2 repeat: matches 2579..2710 of consensus"
repeat_region      13276..13457
                        /note="AluSg/x repeat: matches 129..310 of consensus"
repeat_region      13679..13873
                        /note="MIR repeat: matches 5..213 of consensus"
repeat_region      14132..14206
                        /note="MIR repeat: matches 163..233 of consensus"
repeat_region      14207..14413
                        /note="MER8 repeat: matches 2..239 of consensus"
repeat_region      14414..14548
                        /note="MIR repeat: matches 12..163 of consensus"
repeat_region      14793..15073
                        /note="AluY repeat: matches 1..311 of consensus"
repeat_region      15383..15589
                        /note="MER3 repeat: matches 1..209 of consensus"
repeat_region      16139..16279
                        /note="MER5B repeat: matches 29..178 of consensus"
repeat_region      16317..16466
                        /note="MIR repeat: matches 52..212 of consensus"
repeat_region      16667..17000
                        /note="L1PA9 repeat: matches 5829..6163 of consensus"
repeat_region      17001..17301
                        /note="AluYb8 repeat: matches 1..302 of consensus"
repeat_region      17302..17642
                        /note="L1PA9 repeat: matches 5491..5829 of consensus"
repeat_region      18285..18620
                        /note="2 copies 168 mer 78% conserved"
repeat_region      18772..18981
                        /note="MIR repeat: matches 6..242 of consensus"
repeat_region      18945..19005
                        /note="L2 repeat: matches 2648..2702 of consensus"
repeat_region      20349..20489
                        /note="MIR repeat: matches 1..150 of consensus"
repeat_region      20543..20697
                        /note="MER5A repeat: matches 22..188 of consensus"
repeat_region      21496..21830
                        /note="L1MC4 repeat: matches 7477..7849 of consensus"
repeat_region      22420..22650
```

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                    /note="MER46A repeat: matches 1..236 of consensus"
repeat_region   22894..22965
                    /note="3 copies 24 mer 83% conserved"
repeat_region   24309..24606
                    /note="AluSx repeat: matches 1..299 of consensus"
repeat_region   25081..25134
                    /note="27 copies 2 mer ta 70% conserved"
repeat_region   25168..25193
                    /note="13 copies 2 mer tg 100% conserved"
repeat_region   25262..25301
                    /note="20 copies 2 mer tc 90% conserved"
repeat_region   25302..25642
                    /note="L2 repeat: matches 2078..2419 of consensus"
repeat_region   26542..26704
                    /note="MIR repeat: matches 1..160 of consensus"
repeat_region   26822..27057
                    /note="MIR repeat: matches 8..255 of consensus"
repeat_region   28330..28399
                    /note="MIR repeat: matches 82..151 of consensus"
repeat_region   30715..30819
                    /note="MIR repeat: matches 35..138 of consensus"
repeat_region   31196..31319
                    /note="AluJb repeat: matches 2..125 of consensus"
repeat_region   37202..37675
                    /note="L2 repeat: matches 1597..2041 of consensus"
repeat_region   37676..37990
                    /note="AluJb repeat: matches 1..312 of consensus"
repeat_region   37991..38142
                    /note="L2 repeat: matches 2041..2182 of consensus"
repeat_region   38143..38316
                    /note="MER5A repeat: matches 3..189 of consensus"
repeat_region   38317..38464
                    /note="L2 repeat: matches 2182..2419 of consensus"
repeat_region   38676..38801
                    /note="MIR repeat: matches 11..134 of consensus"
repeat_region   38858..38984
                    /note="MIR repeat: matches 123..257 of consensus"
repeat_region   39284..39886
                    /note="L2 repeat: matches 2147..2748 of consensus"
repeat_region   39913..40014
                    /note="MIR repeat: matches 175..262 of consensus"
repeat_region   40015..40311
                    /note="AluSg repeat: matches 1..297 of consensus"
repeat_region   40312..40428
                    /note="MIR repeat: matches 14..175 of consensus"
repeat_region   40667..40774
                    /note="L2 repeat: matches 2616..2702 of consensus"
repeat_region   40776..41088
                    /note="AluSx repeat: matches 1..305 of consensus"
repeat_region   41528..41936
                    /note="L2 repeat: matches 2267..2709 of consensus"
repeat_region   42180..42713
                    /note="L1MB3 repeat: matches 5584..6153 of consensus"
repeat_region   42714..43014
                    /note="AluJb repeat: matches 1..312 of consensus"
repeat_region   43015..43042
                    /note="L1MB3 repeat: matches 6153..6178 of consensus"
```

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repeat_region    43197..43238
                 /note="5S repeat: matches 1..42 of consensus"
repeat_region    43282..43574
                 /note="L2 repeat: matches 2405..2677 of consensus"
repeat_region    45284..45741
                 /note="MLT1C repeat: matches 1..466 of consensus"
repeat_region    45835..45905
                 /note="L2 repeat: matches 1139..1203 of consensus"
repeat_region    45906..46207
                 /note="AluSq repeat: matches 12..313 of consensus"
repeat_region    46208..46584
                 /note="L2 repeat: matches 1203..1621 of consensus"
repeat_region    46714..47015
                 /note="AluSg repeat: matches 1..302 of consensus"
repeat_region    47016..47159
                 /note="MER58B repeat: matches 196..341 of consensus"
repeat_region    47168..47374
                 /note="MER30 repeat: matches 1..230 of consensus"
repeat_region    47427..47581
                 /note="MER61A repeat: matches 4..158 of consensus"
repeat_region    47611..47774
                 /note="AluSx repeat: matches 12..175 of consensus"
repeat_region    48682..48987
                 /note="AluY repeat: matches 1..306 of consensus"
repeat_region    49541..49678
                 /note="L2 repeat: matches 1906..2046 of consensus"
repeat_region    49698..49898
                 /note="MER53 repeat: matches 1..188 of consensus"
repeat_region    49909..49978
                 /note="LTR19B repeat: matches 59..140 of consensus"
repeat_region    50220..50423
                 /note="L2 repeat: matches 2518..2730 of consensus"
repeat_region    50421..50492
                 /note="3 copies 24 mer 93% conserved"
repeat_region    50846..50915
                 /note="MIR repeat: matches 48..117 of consensus"
repeat_region    50914..51068
                 /note="MIR repeat: matches 34..211 of consensus"
repeat_region    51124..51292
                 /note="AluSg/x repeat: matches 130..300 of consensus"
repeat_region    51517..51587
                 /note="MER96 repeat: matches 105..175 of consensus"
repeat_region    52716..52853
                 /note="MIR repeat: matches 68..213 of consensus"
repeat_region    52994..53224
                 /note="MIR repeat: matches 2..258 of consensus"
repeat_region    54036..54154
                 /note="MLT1I repeat: matches 292..410 of consensus"
repeat_region    54234..54586
                 /note="MLT1A2 repeat: matches 1..373 of consensus"
repeat_region    54612..54704
                 /note="MLT1J repeat: matches 106..200 of consensus"
repeat_region    54708..54755
                 /note="L2 repeat: matches 2691..2738 of consensus"
repeat_region    55103..55409
                 /note="AluYb8 repeat: matches 1..314 of consensus"
repeat_region    55876..56326
```

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                          /note="L2 repeat: matches 2225..2658 of consensus"
      repeat_region    56404..56697
                          /note="AluSg repeat: matches 1..292 of consensus"
      repeat_region    56760..56882
                          /note="L2 repeat: matches 2605..2730 of consensus"
      repeat_region    57036..57226
                          /note="MIR repeat: matches 73..262 of consensus"
      repeat_region    57448..57579
                          /note="L1PA16 repeat: matches 6025..6157 of consensus"
      repeat_region    57817..58128
                          /note="L2 repeat: matches 2434..2746 of consensus"
      repeat_region    58772..59030
                          /note="MIR repeat: matches 1..262 of consensus"
      repeat_region    59040..59091
                          /note="MIR repeat: matches 206..257 of consensus"
      repeat_region    59050..59118
                          /note="L2 repeat: matches 2626..2729 of consensus"
      repeat_region    59465..59797
                          /note="AluSx repeat: matches 1..301 of consensus"
      repeat_region    61554..61833
                          /note="AluSx repeat: matches 6..286 of consensus"
      repeat_region    62011..62239
                          /note="MIR repeat: matches 2..242 of consensus"
      repeat_region    62265..62379
                          /note="L2 repeat: matches 2430..2545 of consensus"
      repeat_region    63472..63529
                          /note="MIR repeat: matches 185..242 of consensus"
      repeat_region    64262..64313
                          /note="MIR repeat: matches 92..143 of consensus"
      repeat_region    64330..64409
                          /note="MER33 repeat: matches 241..324 of consensus"
      repeat_region    64459..64631
                          /note="L1MA10 repeat: matches 5999..6322 of consensus"
      repeat_region    64637..64862
                          /note="MER33 repeat: matches 5..225 of consensus"
      repeat_region    65788..66082
                          /note="AluJo repeat: matches 6..304 of consensus"
      repeat_region    66968..66991
                          /note="L2 repeat: matches 2470..2493 of consensus"
      repeat_region    67036..67653
                          /note="L2 repeat: matches 1882..2511 of consensus"
      repeat_region    67654..67700
                          /note="L1PA16 repeat: matches 4148..4193 of consensus"
      repeat_region    67701..67998
                          /note="AluY repeat: matches 1..296 of consensus"
      repeat_region    67999..68463
                          /note="L1PA16 repeat: matches 4193..4655 of consensus"
      repeat_region    68464..68826
                          /note="THE1B repeat: matches 1..364 of consensus"
      repeat_region    68827..70335
                          /note="L1PA16 repeat: matches 4655..6143 of consensus"
      repeat_region    70349..70538
                          /note="L2 repeat: matches 1697..1895 of consensus"
      repeat_region    70565..70865
                          /note="AluY repeat: matches 1..305 of consensus"
      repeat_region    70932..71126
                          /note="L1ME3 repeat: matches 5734..5939 of consensus"
```

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repeat_region    71385..71690
                 /note="AluYa5 repeat: matches 1..310 of consensus"
repeat_region    71717..72253
                 /note="MLT1F repeat: matches 11..513 of consensus"
repeat_region    72615..72631
                 /note="MIR repeat: matches 196..212 of consensus"
repeat_region    72632..72870
                 /note="MER8 repeat: matches 1..239 of consensus"
repeat_region    72871..73028
                 /note="MIR repeat: matches 45..196 of consensus"
repeat_region    73892..73979
                 /note="MIR repeat: matches 59..147 of consensus"
repeat_region    74431..74484
                 /note="27 copies 2 mer ca 96% conserved"
repeat_region    74436..74483
                 /note="2 copies 24 mer 100% conserved"
repeat_region    74504..74671
                 /note="MIR repeat: matches 2..171 of consensus"
repeat_region    75019..75185
                 /note="L2 repeat: matches 2517..2704 of consensus"
repeat_region    75149..75249
                 /note="MIR repeat: matches 28..137 of consensus"
repeat_region    75397..75588
                 /note="MLT1A1 repeat: matches 1..194 of consensus"
repeat_region    75646..75831
                 /note="MLT1A1 repeat: matches 171..365 of consensus"
repeat_region    76554..76826
                 /note="AluSg1 repeat: matches 1..308 of consensus"
repeat_region    76863..76903
                 /note="L2 repeat: matches 2652..2693 of consensus"
repeat_region    77089..77189
                 /note="MIR repeat: matches 41..144 of consensus"
repeat_region    77359..77679
                 /note="AluSx repeat: matches 1..301 of consensus"
repeat_region    78584..78722
                 /note="L2 repeat: matches 2615..2750 of consensus"
repeat_region    79058..79304
                 /note="MIR repeat: matches 8..262 of consensus"
repeat_region    81458..81515
                 /note="MIR repeat: matches 95..154 of consensus"
repeat_region    81526..81665
                 /note="L2 repeat: matches 2352..2503 of consensus"
repeat_region    81793..81843
                 /note="L2 repeat: matches 2706..2750 of consensus"
repeat_region    82019..82082
                 /note="MIR repeat: matches 90..153 of consensus"
repeat_region    82664..82739
                 /note="L2 repeat: matches 2647..2722 of consensus"
repeat_region    82740..83045
                 /note="AluSx repeat: matches 1..312 of consensus"
repeat_region    83046..83071
                 /note="L2 repeat: matches 2722..2747 of consensus"
repeat_region    83813..83946
                 /note="MIR repeat: matches 89..250 of consensus"
repeat_region    83904..83954
                 /note="L2 repeat: matches 2648..2698 of consensus"
repeat_region    83963..84024
```

```
                    /note="MIR repeat: matches 77..140 of consensus"
repeat_region    84133..84258
                    /note="MIR repeat: matches 7..136 of consensus"
repeat_region    84602..84697
                    /note="MIR repeat: matches 49..135 of consensus"
repeat_region    85012..85350
                    /note="MLT1A2 repeat: matches 1..340 of consensus"
repeat_region    85365..85456
                    /note="MIR repeat: matches 33..128 of consensus"
repeat_region    85526..85776
                    /note="MIR repeat: matches 7..262 of consensus"
repeat_region    85935..86011
                    /note="MER58A repeat: matches 42..121 of consensus"
repeat_region    86101..86173
                    /note="MER58A repeat: matches 143..219 of consensus"
repeat_region    87299..87643
                    /note="AluYb8 repeat: matches 1..310 of consensus"
repeat_region    88003..88303
                    /note="AluSx repeat: matches 1..301 of consensus"
repeat_region    92655..92799
                    /note="L1MC5 repeat: matches 7720..7866 of consensus"
repeat_region    99017..99109
                    /note="L2 repeat: matches 2388..2488 of consensus"
repeat_region    99392..99521
                    /note="L2 repeat: matches 2576..2710 of consensus"
repeat_region    99694..99834
                    /note="L2 repeat: matches 2610..2750 of consensus"
repeat_region    100051..100090
                    /note="20 copies 2 mer tt 80% conserved"
repeat_region    100093..100400
                    /note="AluSx repeat: matches 3..312 of consensus"
repeat_region    100764..100931
                    /note="MER3 repeat: matches 3..207 of consensus"
repeat_region    101144..101446
                    /note="AluJo repeat: matches 1..292 of consensus"
repeat_region    101798..101867
                    /note="L2 repeat: matches 2672..2744 of consensus"
repeat_region    101952..102471
                    /note="MER1A repeat: matches 6..527 of consensus"
repeat_region    102850..103006
                    /note="MIR repeat: matches 20..168 of consensus"
repeat_region    103007..103052
                    /note="MLT1A1 repeat: matches 1..51 of consensus"
repeat_region    103053..103356
                    /note="AluSp repeat: matches 1..303 of consensus"
repeat_region    103357..103729
                    /note="MLT1A1 repeat: matches 51..365 of consensus"
repeat_region    103730..103791
                    /note="MIR repeat: matches 168..231 of consensus"
repeat_region    103886..103998
                    /note="MSTA repeat: matches 1..114 of consensus"
repeat_region    103996..104323
                    /note="MSTA repeat: matches 1..388 of consensus"
repeat_region    104372..104503
                    /note="AluY repeat: matches 166..297 of consensus"
repeat_region    104594..104824
                    /note="MIR repeat: matches 10..259 of consensus"
```

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repeat_region    104874..104954
                 /note="L2 repeat: matches 2624..2709 of consensus"
repeat_region    105235..105332
                 /note="MIR repeat: matches 47..145 of consensus"
repeat_region    107333..107459
                 /note="MLT1C repeat: matches 340..466 of consensus"
repeat_region    107460..107589
                 /note="L1MA7 repeat: matches 6159..6288 of consensus"
repeat_region    107590..107718
                 /note="MLT1C repeat: matches 211..340 of consensus"
repeat_region    107755..108017
                 /note="AluJo repeat: matches 18..277 of consensus"
repeat_region    108019..108208
                 /note="MLT1C repeat: matches 1..192 of consensus"
repeat_region    108326..108922
                 /note="L2 repeat: matches 2080..2710 of consensus"
repeat_region    109592..109635
                 /note="22 copies 2 mer gg 75% conserved"
repeat_region    110302..110511
                 /note="L1MA10 repeat: matches 5970..6317 of consensus"
repeat_region    110589..111071
                 /note="L1ME1 repeat: matches 5477..5952 of consensus"
repeat_region    111077..111135
                 /note="L1MB4 repeat: matches 6124..6183 of consensus"
repeat_region    111153..111414
                 /note="L1MB3 repeat: matches 5909..6182 of consensus"
repeat_region    111419..111617
                 /note="L1ME1 repeat: matches 5283..5487 of consensus"
repeat_region    111622..112876
                 /note="L1MB8 repeat: matches 4877..6173 of consensus"
repeat_region    112873..114198
                 /note="L1M4 repeat: matches 3073..4391 of consensus"
repeat_region    114206..115694
                 /note="L1PA2 repeat: matches 4656..6144 of consensus"
repeat_region    115723..116219
                 /note="MLT2CA repeat: matches 1..489 of consensus"
repeat_region    116220..116291
                 /note="3 copies 24 mer 81% conserved"
repeat_region    116283..116348
                 /note="MLT2CA repeat: matches 444..508 of consensus"
repeat_region    116377..118409
                 /note="L1MEc repeat: matches 1212..2985 of consensus"
repeat_region    118410..118683
                 /note="AluY repeat: matches 1..298 of consensus"
repeat_region    118684..118923
                 /note="L1MEc repeat: matches 983..1212 of consensus"
repeat_region    118955..119117
                 /note="MER20 repeat: matches 51..218 of consensus"
repeat_region    119118..119284
                 /note="L1MEc repeat: matches 802..988 of consensus"
repeat_region    119285..119682
                 /note="MLT1A1 repeat: matches 1..365 of consensus"
repeat_region    119683..119810
                 /note="L1MEc repeat: matches 681..802 of consensus"
repeat_region    119830..120493
                 /note="L2 repeat: matches 1734..2603 of consensus"
repeat_region    120522..120894
```

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                    /note="MLT1B repeat: matches 1..426 of consensus"
repeat_region    120923..121042
                    /note="5 copies 24 mer 68% conserved"
repeat_region    121180..121227
                    /note="2 copies 24 mer 95% conserved"
repeat_region    121184..121227
                    /note="22 copies 2 mer gt 100% conserved"
repeat_region    122617..122772
                    /note="MER5A repeat: matches 4..188 of consensus"
repeat_region    122787..122900
                    /note="MER5B repeat: matches 91..173 of consensus"
repeat_region    122901..123193
                    /note="AluJo repeat: matches 4..298 of consensus"
repeat_region    123194..123275
                    /note="MER5B repeat: matches 1..91 of consensus"
repeat_region    123437..124087
                    /note="L2 repeat: matches 1555..2750 of consensus"
repeat_region    124164..124586
                    /note="L2 repeat: matches 57..485 of consensus"
repeat_region    125405..125535
                    /note="Charlie4a repeat: matches 369..495 of consensus"
repeat_region    125536..125695
                    /note="FRAM repeat: matches 2..161 of consensus"
repeat_region    125696..126026
                    /note="Charlie4a repeat: matches 19..369 of consensus"
repeat_region    126098..126459
                    /note="MLT1A1 repeat: matches 1..365 of consensus"
repeat_region    126630..126693
                    /note="L2 repeat: matches 2641..2704 of consensus"
repeat_region    126784..127362
                    /note="L2 repeat: matches 2176..2750 of consensus"
repeat_region    127366..127489
                    /note="MIR repeat: matches 46..185 of consensus"
repeat_region    127679..127826
                    /note="L2 repeat: matches 2552..2691 of consensus"
repeat_region    127827..128126
                    /note="AluJo repeat: matches 4..302 of consensus"
repeat_region    128127..128405
                    /note="L2 repeat: matches 2241..2552 of consensus"
repeat_region    128518..128663
                    /note="L2 repeat: matches 1873..2021 of consensus"
repeat_region    128674..129015
                    /note="MLT1A1 repeat: matches 1..358 of consensus"
repeat_region    129016..129205
                    /note="L2 repeat: matches 1672..1868 of consensus"
repeat_region    129216..129297
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repeat_region    131041..131232
                    /note="AluSg/x repeat: matches 135..292 of consensus"
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repeat_region    131743..132226
                    /note="MLT1G repeat: matches 31..496 of consensus"
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repeat_region    132996..133294
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repeat_region    134184..134313
                 /note="L1P3 repeat: matches 5682..5809 of consensus"
repeat_region    134373..134437
                 /note="L1MA7 repeat: matches 6224..6288 of consensus"
repeat_region    134438..134744
                 /note="MER2 repeat: matches 34..345 of consensus"
repeat_region    134748..134835
                 /note="L1MA6 repeat: matches 6154..6241 of consensus"
repeat_region    134878..135187
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repeat_region    135888..136007
                 /note="L1ME1 repeat: matches 6026..6135 of consensus"
repeat_region    136270..136561
                 /note="AluSx repeat: matches 21..312 of consensus"
repeat_region    136598..136661
                 /note="MIR repeat: matches 69..132 of consensus"
repeat_region    136902..137090
                 /note="MIR repeat: matches 12..206 of consensus"
repeat_region    137099..137227
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repeat_region    137525..137870
                 /note="MLT1D repeat: matches 130..471 of consensus"
repeat_region    137893..138056
                 /note="AluJo repeat: matches 123..301 of consensus"
repeat_region    138057..138345
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repeat_region    138346..138472
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repeat_region    138474..138539
                 /note="MLT1D repeat: matches 440..505 of consensus"
repeat_region    138554..138675
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repeat_region    138694..139033
                 /note="L2 repeat: matches 2362..2692 of consensus"
repeat_region    138993..139044
                 /note="MIR repeat: matches 210..261 of consensus"
repeat_region    139737..139807
                 /note="MLT1C repeat: matches 393..464 of consensus"
repeat_region    139808..139873
                 /note="L1PA8 repeat: matches 6097..6162 of consensus"
repeat_region    139874..140272
                 /note="MLT1C repeat: matches 1..393 of consensus"
repeat_region    140332..140461
                 /note="MER5A repeat: matches 26..189 of consensus"
repeat_region    140611..140903
                 /note="LTR16C repeat: matches 61..387 of consensus"
repeat_region    141410..141594
                 /note="MIR repeat: matches 25..210 of consensus"
repeat_region    142664..142699
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         repeat_region   143339..143662
                        /note="MLT1A1 repeat: matches 6..365 of consensus"
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                        /note="L2 repeat: matches 2593..2702 of consensus"
         repeat_region   145806..145889
                        /note="MIR repeat: matches 37..130 of consensus"
         repeat_region   145957..146261
                        /note="AluSq repeat: matches 1..308 of consensus"
         repeat_region   146264..146376
                        /note="MIR repeat: matches 117..235 of consensus"
         repeat_region   147583..147657
                        /note="L2 repeat: matches 2422..2502 of consensus"
         repeat_region   147859..147978
                        /note="L2 repeat: matches 2616..2750 of consensus"
         repeat_region   148013..148084
                        /note="L2 repeat: matches 2636..2707 of consensus"
         repeat_region   148687..149141
                        /note="LTR16B repeat: matches 1..461 of consensus"
         repeat_region   150442..151102
                        /note="L2 repeat: matches 1490..2109 of consensus"
BASE COUNT
ORIGIN


468 100    0.0
AF195953      Homo sapiens membrane-bound aminopeptidase P (XNPEP2) gene,
              complete cds. 206618 bp, DNA, linear, PRI 26-MAR-2002
ACCESSION     AF195953
VERSION       AF195953.2  GI:19718557
KEYWORDS      .
SOURCE        Homo sapiens (human)
  ORGANISM    Homo sapiens
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE     1  (bases 1 to 206618)
  AUTHORS     Ryan,J.W., Jin,L., Horvath,I. and Sprinkle,T.J.C.
  TITLE       Human membrane-bound aminopeptidase P genomic DNA
  JOURNAL     Unpublished
REFERENCE     2  (bases 1 to 206618)
  AUTHORS     Ryan,J.W., Jin,L., Horvath,I. and Sprinkle,T.J.C.
  TITLE       Direct Submission
  JOURNAL     Submitted (18-OCT-1999) Vascular Biology Center, Medical College of
              Georgia, 1120 15th Street, Augusta, GA 30912, USA
REFERENCE     3  (bases 1 to 206618)
  AUTHORS     Ryan,J.W., Jin,L., Horvath,I. and Sprinkle,T.J.C.
  TITLE       Direct Submission
  JOURNAL     Submitted (26-MAR-2002) Vascular Biology Center, Medical College of
              Georgia, 1120 15th Street, Augusta, GA 30912, USA
  REMARK      Sequence update by submitter
COMMENT       On Mar 26, 2002 this sequence version replaced gi:11066156.
FEATURES             Location/Qualifiers
     source          1..206618
                     /organism="Homo sapiens"
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                          /mol_type="genomic DNA"
                          /db_xref="taxon:9606"
          gene              144189..176791
                          /gene="XNPEP2"
          mRNA              join(144189..144502,147348..147421,149203..149313,
                          150445..150508,151478..151582,151837..151923,
                          152849..152995,155710..155811,156987..157068,
                          157392..157587,158401..158490,159714..159823,
                          160536..160613,161726..161797,164422..164482,
                          165754..165823,166414..166518,167248..167307,
                          167936..168012,172845..172934,173533..176791)
                          /gene="XNPEP2"
                          /product="membrane-bound aminopeptidase P"
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          CDS               join(144454..144502,147348..147421,149203..149313,
                          150445..150508,151478..151582,151837..151923,
                          152849..152995,155710..155811,156987..157068,
                          157392..157587,158401..158490,159714..159823,
                          160536..160613,161726..161797,164422..164482,
                          165754..165823,166414..166518,167248..167307,
                          167936..168012,172845..172934,173533..173727)
                          /gene="XNPEP2"
                          /codon_start=1
                          /product="membrane-bound aminopeptidase P"
                          /protein_id="AAG28480.1"
                          /db_xref="GI:11066157"
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                          /gene="XNPEP2"
                          /note="putative proton shuttle; unclassified site"
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                          /note="divalent metal ligand; metal-binding site"
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          3'UTR             175728..176791
                          /gene="XNPEP2"
BASE COUNT
ORIGIN


467   99    0.0
P_AAH14799   Human cDNA sequence SEQ ID NO:12589. 243 bp, cDNA, PAT 26-JUN-2001
ACCESSION    P_AAH14799
KEYWORDS     GENESEQ; Human; primer; detection; diagnosis; antisense therapy;
          gene therapy;  patent; patentdb (v200414, 01-JUL-2004).
SOURCE       Homo sapiens.
  ORGANISM   Homo sapiens.
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REFERENCE   1 (bases 1 to 2243)
  AUTHORS   Ota,T., Isogai,T., Nishikawa,T., Hayashi,K., Saito,K.,
             Yamamoto,J. Ishii,S., Sugiyama,T., Wakamatsu,A., Nagai,K.,
             Otsuki,T.
  TITLE   Primer sets for synthesizing polynucleotides, particularly the 5602
             full- length cDNAs defined in the specification, and for the
             detection and/or diagnosis of the abnormality of the proteins
             encoded by the full-length cDNAs.
  JOURNAL   Patent: EP1074617-A2; Filing Date: 28-JUL-2000; 2000EP-00116126;
             Publication Date: 07-FEB-2001; Priority: 29-JUL-1999;
             99JP-00248036. 27-AUG-1999;   99JP-00300253. 11-JAN-2000;
             2000JP-00118776. 02-MAY-2000; 2000JP-00183767. 09-JUN-2000;
             2000JP-00241899; Assignee: (HELI-) HELIX RES INST; Cross Reference:
             WPI; 2001-318749/34; Patent Format: Claim 8; SEQ ID NO 12589; 2537pp
             + Sequence Listing; English.
  COMMENT   The present invention describes primer sets for synthesising 5602
             full- length cDNAs defined in the specification. Where a primer set
             comprises: (a) an oligo-dT primer and an oligonucleotide
             complementary to the complementary strand of a polynucleotide which
             comprises one of the 5602 nucleotide sequences defined in the
             specification, where the oligonucleotide comprises at least 15
             nucleotides; or (b) a combination of an oligonucleotide comprising
             a sequence complementary to the complementary strand of a
             polynucleotide which comprises a 5'-end sequence and an
             oligonucleotide comprising a sequence complementary to a
             polynucleotide which comprises a 3'-end sequence, where the
             oligonucleotide comprises at least 15 nucleotides and the
             combination of the 5'-end sequence/3'-end sequence is selected from
             those defined in the specification. The primer sets can be used in
             antisense therapy and in gene therapy. The primers are useful for
             synthesising polynucleotides, particularly full-length cDNAs. The
             primers are also useful for the detection and/or diagnosis of the
             abnormality of the proteins encoded by the full-length cDNAs. The
             primers allow obtaining of the full-length cDNAs easily without any
             specialised methods. AAH03166 to AAH13628 and AAH13633 to AAH18742
             represent human cDNA sequences; AAB92446 to AAB95893 represent human
             amino acid sequences; and AAH13629 to AAH13632 represent
             oligonucleotides, all of which are used in the exemplification of
             the present invention
FEATURES   Location/Qualifiers
BASE COUNT   467 a   630 c   637 g   509 t
ORIGIN

467 99   0.0
AK001855   Homo sapiens cDNA FLJ10993 fis, clone PLACE1002140. 2243 bp,
            mRNA, linear, PRI 30-JAN-2004
ACCESSION   AK001855
VERSION   AK001855.1 GI:7023382
KEYWORDS   oligo capping; fis (full insert sequence).
SOURCE   Homo sapiens (human)
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Ota,T., Suzuki,Y., Nishikawa,T., Otsuki,T., Sugiyama,T., Irie,R.,
            Wakamatsu,A., Hayashi,K., Sato,H., Nagai,K., Kimura,K., Makita,H.,
            Sekine,M., Obayashi,M., Nishi,T., Shibahara,T., Tanaka,T.,

Ishii,S., Yamamoto,J., Saito,K., Kawai,Y., Isono,Y., Nakamura,Y.,
Nagahari,K., Murakami,K., Yasuda,T., Iwayanagi,T., Wagatsuma,M.,
Shiratori,A., Sudo,H., Hosoiri,T., Kaku,Y., Kodaira,H., Kondo,H.,
Sugawara,M., Takahashi,M., Kanda,K., Yokoi,T., Furuya,T.,
Kikkawa,E., Omura,Y., Abe,K., Kamihara,K., Katsuta,N., Sato,K.,
Tanikawa,M., Yamazaki,M., Ninomiya,K., Ishibashi,T., Yamashita,H.,
Murakawa,K., Fujimori,K., Tanai,H., Kimata,M., Watanabe,M.,
Hiraoka,S., Chiba,Y., Ishida,S., Ono,Y., Takiguchi,S., Watanabe,S.,
Yosida,M., Hotuta,T., Kusano,J., Kanehori,K., Takahashi-Fujii,A.,
Hara,H., Tanase,T., Nomura,Y., Togiya,S., Komai,F., Hara,R.,
Takeuchi,K., Arita,M., Imose,N., Musashino,K., Yuuki,H., Oshima,A.,
Sasaki,N., Aotsuka,S., Yoshikawa,Y., Matsunawa,H., Ichihara,T.,
Shiohata,N., Sano,S., Moriya,S., Momiyama,H., Satoh,N., Takami,S.,
Terashima,Y., Suzuki,O., Nakagawa,S., Senoh,A., Mizoguchi,H.,
Goto,Y., Shimizu,F., Wakebe,H., Hishigaki,H., Watanabe,T.,
Sugiyama,A., Takemoto,M., Kawakami,B., Yamazaki,M., Watanabe,K.,
Kumagai,A., Itakura,S., Fukuzumi,Y., Fujimori,Y., Komiyama,M.,
Tashiro,H., Tanigami,A., Fujiwara,T., Ono,T., Yamada,K., Fujii,Y.,
Ozaki,K., Hirao,M., Ohmori,Y., Kawabata,A., Hikiji,T., Kobatake,N.,
Inagaki,H., Ikema,Y., Okamoto,S., Okitani,R., Kawakami,T.,
Noguchi,S., Itoh,T., Shigeta,K., Senba,T., Matsumura,K.,
Nakajima,Y., Mizuno,T., Morinaga,M., Sasaki,M., Togashi,T.,
Oyama,M., Hata,H., Watanabe,M., Komatsu,T., Mizushima-Sugano,J.,
Satoh,T., Shirai,Y., Takahashi,Y., Nakagawa,K., Okumura,K.,
Nagase,T., Nomura,N., Kikuchi,H., Masuho,Y., Yamashita,R.,
Nakai,K., Yada,T., Nakamura,Y., Ohara,O., Isogai,T. and Sugano,S.
  TITLE   Complete sequencing and characterization of 21,243 full-length
            human cDNAs
  JOURNAL   Nat. Genet. 36 (1), 40-45 (2004)
   PUBMED   14702039
REFERENCE   2
  AUTHORS   Isogai,T., Ota,T., Hayashi,K., Sugiyama,T., Otsuki,T., Suzuki,Y.,
            Nishikawa,T., Nagai,K., Sugano,S., Takahashi-Fujii,A., Hara,H.,
            Tanase,T., Nomura,Y., Togiya,S., Komai,F., Hara,R., Takeuchi,K.,
            Arita,M., Nabekura,T., Ishii,S., Kawai,Y., Saito,K., Yamamoto,J.,
            Wakamatsu,A., Nakamura,Y., Nagahari,K., Masuho,Y. and Oshima,A.
  TITLE   NEDO human cDNA sequencing project
  JOURNAL   Unpublished
REFERENCE   3 (bases 1 to 2243)
  AUTHORS   Isogai,T. and Otsuki,T.
  TITLE   Direct Submission
  JOURNAL   Submitted (16-FEB-2000) Takao Isogai, Helix Research Institute,
            Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
            (E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
COMMENT   NEDO human cDNA sequencing project supported by Ministry of
            International Trade and Industry of Japan; cDNA full insert
            sequencing: Research Association for Biotechnology; cDNA library
            construction, 5'- & 3'-end one pass sequencing and clone selection:
            Helix Research Institute (supported by Japan Key Technology Center
            etc.) and Department of Virology, Institute of Medical Science,
            University of Tokyo.
FEATURES   Location/Qualifiers
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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="PLACE1002140"

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                    /tissue_type="placenta"
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                    /codon_start=1
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                    /db_xref="GI:7023383"
BASE COUNT
ORIGIN

449  98   0.0
AX332625     Sequence 3134 from Patent WO0194629. 458 bp,
          DNA, linear, PAT 09-JAN-2002
ACCESSION    AX332625
VERSION      AX332625.1  GI:18123259
KEYWORDS     .
SOURCE       Homo sapiens (human)
  ORGANISM   Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1
  AUTHORS    Young,P.E., Augustus,M., Carter,K.C., Ebner,R., Endress,G.,
          Horrigan,S., Soppet,D.R. and Weaver,Z.
  TITLE      Cancer gene determination and therapeutic screening using signature
          gene sets
  JOURNAL    Patent: WO 0194629-A 3134 13-DEC-2001;
          Avalon Pharmaceuticals (US)
FEATURES             Location/Qualifiers
     source          1..458
                    /organism="Homo sapiens"
                    /mol_type="unassigned DNA"
                    /db_xref="taxon:9606"
BASE COUNT
ORIGIN

449  98   0.0
AX332852     Sequence 3361 from Patent WO0194629. 458 bp,
          DNA, linear, PAT 09-JAN-2002
ACCESSION    AX332852
VERSION      AX332852.1  GI:18123486
KEYWORDS     .
SOURCE       Homo sapiens (human)
  ORGANISM   Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1
  AUTHORS    Young,P.E., Augustus,M., Carter,K.C., Ebner,R., Endress,G.,
          Horrigan,S., Soppet,D.R. and Weaver,Z.
  TITLE      Cancer gene determination and therapeutic screening using signature
          gene sets
  JOURNAL    Patent: WO 0194629-A 3361 13-DEC-2001;
          Avalon Pharmaceuticals (US)
FEATURES             Location/Qualifiers
     source          1..458
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                    /mol_type="unassigned DNA"
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                    /db_xref="taxon:9606"
BASE COUNT
ORIGIN
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Dayhoff Protein Database (Rel 78, Mar 2004)

P_AAB87540 Human PRO831 - Homo sapiens.
Length: 73 aa
Accession: P_AAB87540;
Species: Homo sapiens.
Keywords: Human; PRO protein; mapping; patent; GENESEQ patentdb.
Patent number: WO200116318-A2.
Publication date: 08-MAR-2001.
Filing date: 24-AUG-2000; 2000WO-US023328.
Priority: 01-SEP-1999; 99WO-US020111. 15-SEP-1999; 99WO-US021090.
        07-DEC-1999; 99US-0169495P. 09-DEC-1999; 99US-0170262P.
        11-JAN-2000; 2000US-0175481P. 18-FEB-2000; 2000WO-US004341.
        18-FEB-2000; 2000WO-US004342. 22-FEB-2000; 2000WO-US004414.
        01-MAR-2000; 2000WO-US005601. 03-MAR-2000; 2000US-0187202P.
        21-MAR-2000; 2000US-0191007P. 30-MAR-2000; 2000WO-US008439.
        25-APR-2000; 2000US-0199397P. 22-MAY-2000; 2000WO-US014042.
        05-JUN-2000; 2000US-0209832P.
Assignee: (GETH) GENENTECH INC.
Inventors: Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
        Grimaldi CJ, Gurney AL, Watanabe CK, Wood WI;
Cross reference: WPI; 2001-183260/18. N-PSDB; AAF92072.
Title: Eighty four nucleic acids encoding PRO polypeptides, useful in
        molecular biology, including use as hybridization probes, and in
        chromosome and gene mapping.
Patent format: Claim 12; Fig 30; 278pp; English.
Comment: The present sequence is a human PRO polypeptide (secreted and
        transmembrane). The PRO protein, and PRO agonists, PRO antagonists
        or anti-PRO antibodies are useful for preparation of a medicament
        useful in the treatment of a condition which is responsive to the
        PRO protein, agonists, antagonists or anti-PRO antibodies. The PRO
        protein may also be employed as molecular weight markers for
        protein electrophoresis. The PRO coding sequence has applications
        in molecular biology, including use as hybridisation probes, and in
        chromosome and gene mapping
Database: GENESEQ patent database (v200414, 01-JUL-2004).

P_AAY99346 Human PRO831 (UNQ471) amino acid sequence SEQ ID NO:22 - Homo
        sapiens.
Length: 73 aa
Accession: P_AAY99346;
Species: Homo sapiens.
Keywords: Human; PRO polypeptide; membrane bound protein; receptor;
        diagnosis; transmembrane; secretion; immunoadhesion;
        pharmaceutical; screening; patent; GENESEQ patentdb.
Patent number: WO200012708-A2.
Publication date: 09-MAR-2000.
Filing date: 01-SEP-1999; 99WO-US020111.
Priority: 01-SEP-1998; 98US-0098716P. 01-SEP-1998; 98US-0098749P.
        01-SEP-1998; 98US-0098750P.18-NOV-1998; 98US-0108858P. 18-NOV-1998;
        98US-0108904P. plus 119 more dates.
Assignee: (GETH) GENENTECH INC.
Inventors: Baker K, Goddard A, Gurney AL, Smith V, Watanabe CK, Wood WI;
Cross reference: WPI; 2000-237871/20. N-PSDB; AAA37028.
Title: New mammalian DNA sequences encoding transmembrane, receptor or
        secreted PRO polypeptides, useful for screening of potential
        peptide or small molecule inhibitors of the relevant

receptor/ligand interactions.
Patent format: Claim 12; Fig 14; 773pp; English.
Comment: AAA37022 to AAA37144 encode the new isolated human transmembrane,
    receptor or secreted PRO polypeptides given in AAY99340 to
    AAY99462. The transmembrane and receptor PRO proteins can be used
    for screening of potential peptide or small molecule inhibitors of
    the relevant receptor/ligand interactions. The polypeptides and
    nucleotide sequences encoding then have various industrial
    applications, including uses as pharmaceutical and diagnostic
    agents. AAA37145 to AAA37330 represent PCR primers and
    hybridisation probes used in the isolation of the PRO polypeptides
    from the present invention
Database: GENESEQ patent database (v200414, 01-JUL-2004).